

Art Unit: 1652

APPENDIX A

US-09-746-491-21
; Sequence 21, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-746-491-21

Alignment Scores:

Pred. No.:	4.05e-127	Length:	1216
Score:	1051.00	Matches:	212
Percent Similarity:	68.39%	Conservative:	0
Best Local Similarity:	68.39%	Mismatches:	0
Query Match:	94.68%	Indels:	98
DB:	9	Gaps:	1

US-10-074-978A-24 (1-212) x US-09-746-491-21 (1-1216)

```
Qy      1 ValGlyAlaAlaValPheAspAlaLeuGluSerGluAlaGluSerGlyArgGlnArgLeu 20
      |||
Db      61 GTGGGCGCTGCTGTCTTCGACGCGCTCGAGTCCGAGGCGGAAAGCGGCCGCGCAGCGACTG 120

Qy      21 LeuValGlnLysArgGlyAlaLeuArgArgLysPheGlyPheSerAlaGluAspTyrArg 40
      |||
Db     121 CTGGTCCAGAAGCGGGGCGCTCTCCGAGGGAAGTTCGGCTTCTCGGCCGAGGACTACCGC 180

Qy      41 GluLeuGluArgLeuAlaLeuGlnAlaGluProHisArgAlaGlyArgGlnTrpLysPhe 60
      |||
Db     181 GAGCTGGAGCGCCTGGCGCTCCAGGCTGAGCCCCACCGCGCCGGCCGAGTGGAAAGTTC 240

Qy      61 ProGlySerPheTyrPheAlaIleThrValIleThrThrIleGluTyrGlyHisAlaAla 80
      |||
Db     241 CCCGGCTCCTTCTACTTCGCCATCACCGTCATCACTACCATCGAGTACGGCCACGCCGCG 300

Qy      81 ProGlyThrAspSerGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeu 100
      |||
Db     301 CCGGTACGGACTCCGGCAAGGTCTTCTGCATGTTCTACGCGCTCCTGGGCATCCCGCTG 360

Qy     101 ThrLeuValThrPheGlnSerLeuGlyGluArgLeuAsnAlaValValArgArgLeuLeu 120
      |||
Db     361 ACGCTGGTCACTTTCCAGAGCCTGGGCGAACGGCTGAACGCGGTGGTGCGGCGCCTCCTG 420

Qy     121 LeuAlaAlaLysCysCysLeuGlyLeuArgTrpThrCysValSerThrGluAsnLeuVal 140
      |||
Db     421 TTGGCGGCCAAGTGCTGCTGGGCTGCGGTGGACGTGCGTGTCACGGAGAACCTGGTG 480

Qy     141 ValAlaGlyLeuLeuAlaCysAlaAlaThrLeuAlaLeuGlyAlaValAlaPheSerHis 160
      |||
Db     481 GTGGCCGGGCTGCTGGCGTGTGCCGCCACCTGGCCCTCGGGGCCGTCGCCTTCTCGCAC 540

Qy     161 PheGluGlyTrpThrPhePheHisAlaTyrTyrTyrCysPheIleThrLeuThrThrIle 180
      |||
Db     541 TTCGAGGGCTGGACCTTCTTCCACGCCTACTACTGCTTCATCACCTCACCACCATC 600

Qy     181 GlyPheGly----- 183
```

```

      |||
Db    601 GGCTTCGGCGACTTCGTGGCACTGCAGAGCGGCCAGGCGCTGCAGAGGAAGCTCCCCTAC 660
Qy    183 ----- 183
Db    661 GTGGCCTTCAGCTTCCTCTACATCCTCCTGGGGCTCACGGTCATTGGCGCCTTCCTCAAC 720
Qy    183 ----- 183
Db    721 CTGGTGGTCTCGCGCTTCCTCGTTGCCAGCGCCGACTGGCCCAGCGCGCTGCCCGCACC 780
Qy    183 ----- 183
Db    781 CCCAGCCCGCGCCCCCGGGGGCGCCCGAGAGCCGTGGCCTCTGGCTGCCCGCCGCCCG 840
Qy    183 ----- 183
Db    841 GCCCGCTCCGTGGGCTCCGCCTCTGTCTTCTGCCACGTGCACAAGCTGGAGAGGTGCGCC 900
Qy    184 ---AspAsnLeuGlyPheSerProProSerSerProGlyValValArgGlyGlyGlnAla 202
      |||
Db    901 CGCGACAACCTGGGCTTTTCGCCCCCTCGAGCCCGGGGTCGTGCGTGGCGGGCAGGCT 960
Qy    203 ProArgLeuGlyAlaArgTrpLysSerIle 212
      |||
Db    961 CCCAGGCTTGGGGCCCGGTGGAAGTCCATC 990
```